09/780,575

```
     (FILE 'HOME' ENTERED AT 13:28:19 ON 27 JUL 2004)

     FILE 'CAPLUS' ENTERED AT 13:30:17 ON 27 JUL 2004
L1          2850 S ICS
L2             0 S L1 AND GAL180
L3             0 S L1 AND NTA
L4             5 S L1 AND REPRESSOR?
L5            31 S LEPB
L6             1 S L1 AND L5

     FILE 'REGISTRY' ENTERED AT 13:40:00 ON 27 JUL 2004
L7             1 S NEAYVHDGPVRSLN/SQSP

     FILE 'CAPLUS, TOXCENTER, USPATFULL' ENTERED AT 13:40:45 ON 27 JUL 2004
L8             3 S L7
L9             1 DUP REM L8 (2 DUPLICATES REMOVED)
L10          112 S (INTERLEUKIN)(3A)(CONVERTASE?)
L11           14 S L10 AND REPRESSOR?
L12           14 DUP REM L11 (0 DUPLICATES REMOVED)

     FILE 'REGISTRY' ENTERED AT 13:44:55 ON 27 JUL 2004
L13           38 S KARKEAELAAATAEQ/SQSP

     FILE 'CAPLUS' ENTERED AT 13:45:17 ON 27 JUL 2004
L14           26 S L13
L15           26 DUP REM L14 (0 DUPLICATES REMOVED)
L16         1147 S (LAMBDA)(3A)(REPRESSOR?)
L17           49 S L16 AND (ANTIGEN? OR EPITOPE?)
L18            1 S L17 AND LIBRAR?
L19          107 S L16 AND PEPTIDE?
L20            5 S L19 AND LIBRAR?
L21            5 DUP REM L20 (0 DUPLICATES REMOVED)

     FILE 'CAPLUS, EMBASE, BIOSIS, MEDLINE, WPIDS' ENTERED AT 13:52:51 ON 27
     JUL 2004
L22          355 S (KODADEK, T? OR KODADEK T?)/AU,IN
L23           24 S L22 AND REPRESSOR?
L24           16 DUP REM L23 (8 DUPLICATES REMOVED)
L25        44384 S LACZ
L26         2676 S L25 AND REPRESSOR?
L27          343 S L26 AND LAMBDA
L28           21 S L27 AND (PEPTID? OR PEPTOID? OR EPITOPE?)
L29           12 DUP REM L28 (9 DUPLICATES REMOVED)
L30       258773 S (DNA OR CIS)(3A)(BINDING)
L31         3989 S L30 AND OPERATOR?
L32          511 S L31 AND FUSION?
L33          392 S L32 AND (PEPTIDE? OR PROTEIN?)(3A)(INTERACT? OR BIND?)
L34            0 S L33 AND (B-GAL?)
L35           84 S L33 AND (LAC?)(3A)(OPERON? OR OPERATOR?)
L36           64 S L35 AND REPRESSOR?
L37           39 DUP REM L36 (25 DUPLICATES REMOVED)
L38           18 S (REPRESSOR?)(3A)(RECONSTIT?)
L39            9 DUP REM L38 (9 DUPLICATES REMOVED)

=>
```

L18 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1993:464906 CAPLUS
DN 119:64906
TI Generation and selection of novel DNA-binding proteins
IN Ladner, Robert C.; Guterman, Sonia K.; Kent, Rachel B.; Ley, Arthur C.
PA Protein Engineering Corp., USA
SO U.S., 145 pp. Cont.-in-part of U.S. 5,096,815.
CODEN: USXXAM
DT Patent
LA English
FAN.CNT 2

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 5198346	A	19930330	US 1990-558011	19900726
	US 5096815	A	19920317	US 1989-293980	19890106
	AU 9049588	A1	19900813	AU 1990-49588	19900105
	EP 452413	A1	19911023	EP 1990-902453	19900105
	EP 452413	B1	20000412		
	R: AT, BE, CH, DE, DK, ES, FR, GB, IT, LI, LU, NL, SE				
	JP 04504052	T2	19920723	JP 1990-502436	19900105
	AT 191746	E	20000415	AT 1990-902453	19900105
PRAI	US 1989-293980	A2	19890106		
	WO 1990-US24	A	19900105		

=> d ab

L18 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2004 ACS on STN
AB A method for selecting a pair of genes encoding proteins that bind to homooligomeric DNA (DBPs) and that associate to form a hybrid hetero-oligomeric protein that binds to a predetd. nonpalindromic, double-stranded DNA target sequence is described. The genes are selected in cells that have first been transformed with a selection vector containing 2 operons, each operon containing a promoter, a target sequence, and a selectable or screenable gene. These cells are also transformed with a 2nd vector containing a DBP gene that has been mutagenized by a non-specific process. Binding of a DBP analog produced by the mutant gene to the target sequence gives the cell a selective advantage; alternatively, the expression of the screenable gene is blocked. The method was used to modify the phage .**lambda**. Cro **repressor** to enable it to bind to an HIV-1 sequence. The selection system comprised a selectable gene, aadA (which confers spectinomycin resistance), and a screenable gene, tet. The operon containing the selectable gene consisted of the aadA gene with its natural promoter and occluding promoter Pcon followed by the target sequence. Upon binding of a DBP to the target sequence, expression from Pcon is inhibited and aadA is expressed. Tet gene expression was driven by Pneo.

=>

L21 ANSWER 1 OF 5 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2002:933401 CAPLUS
DN 138:249140
TI Screening **peptide**/protein **libraries** fused to the . **lambda**. **repressor** DNA-binding domain in E. coli cells
AU Marino-Ramirez, Leonardo; Campbell, Lisa; Hu, James C.
CS Center for Macromolecular Design, Department of Biochemistry and Biophysics, Texas A&M University, College Station, TX, USA
SO Methods in Molecular Biology (Totowa, NJ, United States) (2003), 205(E. coli Gene Expression Protocols), 235-250
CODEN: MMBIED; ISSN: 1064-3745
PB Humana Press Inc.
DT Journal
LA English
RE.CNT 26 THERE ARE 26 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L21 ANSWER 2 OF 5 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1999:450862 CAPLUS
DN 131:83957
TI Interaction trap assay and its reagents
IN Dove, Simon; Joung, J. Keith; Hochschild, Ann
PA President & Fellows of Harvard College, USA
SO U.S., 28 pp.
CODEN: USXXAM
DT Patent
LA English
FAN.CNT 2

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 5925523	A	19990720	US 1997-920015	19970826
	US 6200759	B1	20010313	US 1999-296204	19990421
PRAI	US 1996-24484P	P	19960823		
	US 1997-918612	B2	19970822		
	US 1997-920015	A1	19970826		

RE.CNT 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L21 ANSWER 3 OF 5 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1999:274931 CAPLUS
DN 131:111988
TI Genetic selection of short **peptides** that support protein oligomerization in vivo
AU Zhang, Zhiwen; Murphy, Anne; Hu, James C.; Kodadek, Thomas
CS Department of Chemistry and Biochemistry, University of Texas at Austin, Austin, TX, 78712, USA
SO Current Biology (1999), 9(8), 417-420
CODEN: CUBLE2; ISSN: 0960-9822
PB Current Biology Publications
DT Journal
LA English
RE.CNT 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L21 ANSWER 4 OF 5 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1999:760778 CAPLUS
DN 132:147291
TI A genetic screen to identify sequences that mediate protein oligomerization in Escherichia coli
AU Jappelli, Roberto; Brenner, Sydney
CS Molecular Sciences Institute, Berkeley, CA, 94704, USA
SO Biochemical and Biophysical Research Communications (1999), 266(1), 243-247

CODEN: BBRCA9; ISSN: 0006-291X
PB Academic Press
DT Journal
LA English
RE.CNT 21 THERE ARE 21 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L21 ANSWER 5 OF 5 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1998:151232 CAPLUS
DN 128:201791
TI An interaction trap assay system using the .**lambda**.
repressor for use in a bacterial host
IN Dove, Simon; Joung, J. Keith; Hochschild, Ann
PA President and Fellows of Harvard College, USA
SO PCT Int. Appl., 63 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 2

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9807845	A1	19980226	WO 1997-US14860	19970822
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
AU 9741596	A1	19980306	AU 1997-41596	19970822
PRAI US 1996-24484P	P	19960823		
WO 1997-US14860	W	19970822		

RE.CNT 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

=> d 5 ab

L21 ANSWER 5 OF 5 CAPLUS COPYRIGHT 2004 ACS on STN
AB An interaction trap or two-hybrid system designed for use in a prokaryotic, i.e. bacterial, host is described. The system is generally similar to those designed for use with yeast but using components derived solely from prokaryotes. In particular a system using fusion proteins of the .**lambda**. cI **repressor** that bind an OR2 operator in a modified lacP/O promoter-operator region is described. The second component of the binding assay may be a fusion protein of the α or ω subunits of the bacterial RNA polymerase. Alternatively, the LexA repressor may be used in combination with the SOS box.

L24 ANSWER 13 OF 16 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 5
AN 1998:435315 CAPLUS
DN 129:157351
ED Entered STN: 15 Jul 1998
TI Small-molecule-based strategies for controlling gene expression
AU Denison, Carilee; **Kodadek, Thomas**
CS Center for Biomedical Inventions, Departments of Internal Medicine and Biochemistry, University of Texas Southwestern Medical Center, Dallas, TX, 75235-8573, USA
SO Chemistry & Biology (1998), 5(6), R129-R145
CODEN: CBOLE2; ISSN: 1074-5521
PB Current Biology Ltd.
DT Journal; General Review
LA English
CC 3-0 (Biochemical Genetics)
Section cross-reference(s): 1, 6
AB A review with 110 refs. A central goal in chemical biol. is to gain control over biol. pathways using small mols., and the mRNA-synthesizing machinery is a particularly important target. New advances in our understanding of transcriptional regulation suggests strategies to manipulate these pathways using small mols.
ST gene expression regulation small mol review; transcription factor signal transduction regulation review
IT Proteins, specific or class
RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(DNA-binding, small-mol.-based strategies for controlling gene expression)
IT Immunosuppressants
(effect on gene expression; small-mol.-based strategies for controlling gene expression)
IT Gene
(expression; small-mol.-based strategies for controlling gene expression)
IT DNA
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(interaction with proteins; small-mol.-based strategies for controlling gene expression)
IT Transcription factors
RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(**repressors**; small-mol.-based strategies for controlling gene expression)
IT Proteins, specific or class

L29 ANSWER 2 OF 12 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1999:385780 CAPLUS
DN 131:165864
TI A two-hybrid dual bait system to discriminate specificity of protein interactions
AU Serebriiskii, Ilya; Khazak, Vladimir; Golemis, Erica A.
CS Division of Basic Science, Fox Chase Cancer Center, Philadelphia, PA, 19111, USA
SO Journal of Biological Chemistry (1999), 274(24), 17080-17087
CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology
DT Journal
LA English
AB Biol. regulatory systems require the specific organization of proteins into multicomponent complexes. Two hybrid systems have been used to identify novel components of signaling networks based on interactions with defined partner proteins. An important issue in the use of two-hybrid systems has been the degree to which interacting proteins distinguish their biol. partner from evolutionarily conserved related proteins and the degree to which observed interactions are specific. We adapted the basic two-hybrid strategy to create a novel dual bait system designed to allow single-step screening of libraries for proteins that interact with protein 1 of interest, fused to DNA binding domain A (LexA), but do not interact with protein 2, fused to DNA binding domain B (.**lambda**. cI). Using the selective interactions of Ras and Krev-1(Rap1A) with Raf, RalGDS, and Krit1 as a model, we systematically compared LexA- and cI-fused baits and reporters. The LexA and cI bait reporter systems are well matched for level of bait expression and sensitivity range for interaction detection and allow effective isolation of specifically interacting protein pairs against a nonspecific background. These reagents should prove useful to refine the selectivity of library screens, to reduce the isolation of false positives in such screens, and to perform directed analyses of sequence elements governing the interaction of a single protein with multiple partners.
RE.CNT 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L37 ANSWER 39 OF 39 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 12
AN 1985:574943 CAPLUS
DN 103:174943
TI Novel method for identifying sequence-specific **DNA-binding proteins**
AU Levens, David; Howley, Peter M.
CS Lab. Pathol., Natl. Cancer Inst., Bethesda, MD, 20205, USA
SO Molecular and Cellular Biology (1985), 5(9), 2307-15
CODEN: MCEBD4; ISSN: 0270-7306
DT Journal
LA English
AB A general method was developed for the enrichment and identification of sequence-specific **DNA binding proteins**. A well-characterized **protein**-DNA **interaction** is used to isolate from crude cellular exts. or fractions thereof **proteins** which **bind** to specific DNA sequences; the method is based solely on this **binding** property of the **proteins**. The DNA sequence of interest, cloned adjacent to the **lac operator** DNA segment is incubated with a lac **repressor**-β-galactosidase **fusion** protein which retains full **operator** and inducer binding properties. The DNA fragment bound to the lac **repressor**-β-galactosidase **fusion** protein is precipitated by the addition of affinity-purified anti-β-galactosidase immobilized on beads. This forms an affinity matrix for any **proteins** which might **interact** specifically with the DNA sequence cloned adjacent to the **lac operator**. When incubated with cellular exts. in the presence of excess competitor DNA, any **protein**(s) which specifically **binds** to the cloned DNA sequence of interest can be cleanly precipitated When isopropyl-β-D-thiogalactopyranoside is added, the lac **repressor** releases the bound DNA, and thus the protein-DNA complex consisting of the specific restriction fragment and any specific **binding protein**(s) is released, permitting the identification of the protein by standard biochem. techniques. The utility of this method is demonstrated with the lambda **repressor**, another well-characterized **DNA-binding protein**, as a model. In addition, with crude prepns. of the yeast mitochondrial RNA polymerase, a 70,000-mol.-weight **peptide** was identified which **binds** specifically to the promoter region of the yeast mitochondrial 14S rRNA gene.

L37 ANSWER 16 OF 39 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1998:388645 CAPLUS
DN 129:51713
TI Ligand detection system and its use in identifying ligands specifically **binding** to **protein** domains
IN Li, Min; Stricker, Nicole L.; Bredt, David S.; Christopherson, Karen S.
PA Johns Hopkins University, USA; Li, Min; Stricker, Nicole L.; Bredt, David S.; Christopherson, Karen S.
SO PCT Int. Appl., 94 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9823781	A1	19980604	WO 1997-US21861	19971126
	W: AU, CA, US				
	RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
	AU 9874109	A1	19980622	AU 1998-74109	19971126
PRAI	US 1996-31793P	P	19961126		
	US 1997-43560P	P	19970415		
	WO 1997-US21861	W	19971126		

AB The present invention relates to novel ligand detection systems and methods of using the systems to identify ligands capable of specifically **binding** orphan **protein** domains. The invention also relates to peptide ligands capable of specifically binding an orphan domain of interest such as the PDZ domain of neuronal nitric oxide synthase (nNOS). Further provided are methods of detecting the peptide ligands and those orphan protein domains capable of specifically **binding** the **peptide** ligands. The present invention is useful for a variety of applications including detecting peptide ligands with therapeutic capacity to treat human diseases. To determine optimal **peptide binding** ligands for the nNOS PDZ domain, a **fusion** protein library was constructed that contained 15 randomized residues at the C-terminus. In this library, a degenerate oligonucleotide encoding the random peptides was fused to the end of the Escherichia coli lac **repressor**. Following expression, the lac **repressor protein binds** to the **lac operator** sequence on the same plasmid linking each randomized 15-mer peptide to the plasmid encoding that peptide. This linkage allowed repeated rounds of selection for specific peptide ligands in the population by affinity purification of peptide-**repressor**-plasmid complexes. Binding affinity was 8-100 nM for 95 out of 150 clones specifically interacting with nNOS-PDZ but not with control. Plasmids from these nNOS-specific clones were sequenced and the deduced peptide amino acid sequences were aligned via their C-termini. The optimal sequence is D-X-V-COOH. A search was made of the D-X-V pattern at the C-terminus of protein sequences in a non-redundant protein database. There were 484 matches in the database.
RE.CNT 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

=>

L37 ANSWER 13 OF 39 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1999:359663 CAPLUS
DN 131:1457
TI Methods for production of recombinant lac **repressor** proteins with altered ligand responsivity
IN Matthews, Kathleen S.; Swint-Kruse, Liskin
PA William Marsh Rice University, USA
SO PCT Int. Appl., 29 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 2

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9927108	A1	19990603	WO 1998-US24949	19981120
	W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	AU 9914673	A1	19990615	AU 1999-14673	19981120
	US 2002193568	A1	20021219	US 2002-197053	20020717
PRAI	US 1997-66213P	P	19971120		
	WO 1998-US24949	W	19981120		
	US 1999-172464P	P	19991217		
	US 2000-554537	A2	20000512		
	US 2000-736836	A2	20001214		

RE.CNT 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

=> d 13 ab

L37 ANSWER 13 OF 39 CAPLUS COPYRIGHT 2004 ACS on STN
AB The present invention provides altered lac **repressor** proteins that recognize the **lactose operator** but have an altered ligand responsivity. The altered lac **repressor proteins** contain a **DNA-binding** domain of the natural lac **repressor protein** and a ligand **binding** domain having a responsivity to an alternate inducer ligand or increased sensitivity to isopropyl-β-D-thiogalactoside (IPTG). The altered ligand responsivity provides that a sugar or other small mol. other than allolactose or IPTG acts as an inducer for the altered lac **repressor** protein or that IPTG acts at lower concns. The altered lac **repressor** proteins can further comprise a tetramerizing domain of the natural lac **repressor** protein. DNA sequences encoding the altered lac **repressor** proteins and bacterial and eukaryotic cells containing altered lac **repressor** proteins are also provided. The invention also provides methods for preparing the altered lac **repressor** proteins including: (1) fusing the **DNA-binding** domain of natural lac **repressor** protein to the N-terminus of a ligand **binding protein** (such as arabinose **binding protein**) having responsivity to a ligand other than allolactose or IPTG or (2) fusing a tetramerizing domain of the natural lac **repressor** protein to the C-terminus of the ligand **binding protein** . The invention also included the amino acid sequences of Escherichia coli lac **repressor** and arabinose-**binding protein**, which were used in constructing the **fusion** protein.

WEST Search History

Hide Items | Restore | Clear | Cancel

DATE: Tuesday, July 27, 2004

Hide?	Set Name	Query	Hit Count
	DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD; PLUR=YES; OP=OR		
☐	L7	L6 not l4	29
☐	L6	L5 and operator$	29
☐	L5	(board)near2(regents)near3(texas)	258
☐	L4	l2 and repressor$	9
☐	L3	L2 and (fusion or fused)near10(peptide$ or protein$)	13
☐	L2	kodadek	45
	DB=USPT; PLUR=YES; OP=OR		
☐	L1	(6613582).pn.	1

END OF SEARCH HISTORY